

GENETIC POPULATION SUBDIVISION IN THE COCONUT CRAB, *BIRGUS LATRO* (ANOMURA: COENOBITIDAE)

The coconut crab (*Birgus latro*), the largest and most terrestrial land crab, is found only on relatively isolated tropical islands in the Indian and Pacific Oceans. In recent years, *Birgus* populations have declined rapidly or disappeared in most parts of their range, due largely to over-harvesting for food. It is clear that a management program is required to protect the future survival of individual populations of this species. Information about population structuring within the species is crucial to the development of a suitable management program. This project is using genetic techniques to study the population structure of *Birgus* throughout its distribution to determine if distinct sub-populations exist and, if so, the location of their boundaries (Lavery *et al.*, in press).

Allozyme electrophoresis was used to examine over 300 specimens of *Birgus* from eight locations: Christmas Island (Indian Ocean), the Solomon Islands, Niue, the Cook Islands and four islands in Vanuatu (Tegua, Hiu, Loh and Espiritu Santo). Initially 76 enzyme systems were screened for genetic variation, resulting in the detection of 54 monomorphic loci and 7 polymorphic loci. These polymorphic loci were analysed for allele frequency differences between locations using contingency chi-square analyses. Analyses were performed at different levels of the sampling hierarchy. At the lowest level of the hierarchy, between adjacent islands (the Torres Islands in Vanuatu: Tegua, Hiu and Loh), no significant difference in allele frequencies was found. Similarly, no significant differences were found at the next two levels of the sampling hierarchy, i.e. between islands in a group (the Torres Islands and Espiritu Santo in Vanuatu) and between adjacent island groups (Vanuatu and the Solomon Islands). However, when all the Pacific Ocean samples were compared, there was significant variation in allele frequencies ($P < 0.01$), with individuals from Niue being most variant. Finally, a comparison of samples from the Pacific with those from Christmas Island showed highly significant genetic differences ($P < 0.001$).

A good summary of the genetic differences between locations is shown in a dendrogram of genetic distances (Fig. 1). This clearly shows that all the islands in the Vanuatu and Solomon Islands groups are quite similar. The Cook Islands and, in particular, Niue, are somewhat different from the Vanuatu/Solomon Islands group, but this level of differentiation is much smaller than that with Christmas Island.

The population genetic structure of *Birgus* is also being analysed using mitochondrial DNA (mtDNA) variation. So far, the mtDNA of approximately 50 individuals from four locations (Christmas Island, the Philippines, the Solomon Islands and Niue) has been analysed using 9 different restriction enzymes. Preliminary analysis shows that over 20 differ-

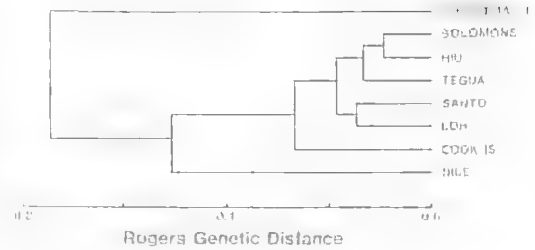


FIG. 1. Dendrogram of genetic relatedness of *Birgus* collections.

ent haplotypes exist among these individuals and, significantly, no haplotype has been found to occur in more than one location. The phylogeny of these haplotypes also suggests that there exists significant geographic structure in the mtDNA variation. Such information about genetic differences between sub-populations may be interpreted in terms of the level of genetic drift or the rates of larval migration between sub-populations. Using the allozyme data alone, and interpreting these data by Slatkin's private alleles method, a migration rate between Christmas Island and the Solomon Islands of 0.3 individuals per generation was calculated. As the *Birgus* generation time may be 12 years, this would represent a migration of one individual every 40 years. In comparison, the rate of migration between the Pacific Islands was calculated to be approximately an order of magnitude less, at 3 individuals per generation, or about one individual every four years.

Although this study is not yet complete, the findings so far suggest that significant genetic population subdivision exists in *Birgus*. This may have important consequences for both the future management of the species and also any future artificial rearing of the coconut crab. In addition, the pattern of larval dispersal found in *Birgus* may be closely related to that of other species in this region with planktonic larvae.

Acknowledgements

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Literature Cited

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